(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a second specificity ligand, wherein said specificity ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said first specificity ligand and said second specificity ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

16. (Amended) The method of claim 15, wherein said enzyme family is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

17. (Amended) The method of claim 15, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

18. (Amended) The method of claim 15, wherein said common ligand and said specificity ligands are attached by a linker having approximate C2 symmetry.

D1 Contd

19. The method of claim 18, wherein said linker has perfect C2 symmetry.

Please add the following new claims.

D2

37. (New) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand, wherein said common ligand competes for cofactor binding to an enzyme in an enzyme family, and a first specificity ligand, wherein said specificity ligand binds to a substrate binding site of said first enzyme, wherein said enzyme family comprises two or more enzymes that bind to the same cofactor;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a second specificity ligand, wherein said specificity ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said first specificity ligand and said second specificity ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

38. (New) The method of claim 37, wherein said enzyme family is selected from the group consisting of kinases,

D2 Cont'd

dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

39. (New) The method of claim 37, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

40. (New) The method of claim 37, wherein said common ligand and said specificity ligands are attached by a linker having approximate C2 symmetry.

41. (New) The method of claim 40, wherein said linker has perfect C2 symmetry.

REMARKS

Claims 15-19 are pending. Claims 15-19 have been amended. New claims 37-41 have been added. Support for the amendments and new claims can be found throughout the specification and in the claims as filed. In particular, support for the amendment to claim 15 can be found, for example, on page 8, lines 29-31; page 11, lines 6-13; page 13, line 32, to page 14, line 2; page 15, lines 1-13; page 31, lines 23-33; and page